

Amendments to the Claims

Please cancel claims 2, 10, 12, 14-22, 24, 27-35, 37, 39-43, 45-47 and 49-77 without prejudice.

Please amend claims 1, 3, 4, 9, 11, 12, 23, 25, 26 36, and 38.

Please add new claims 78-81.

Upon entry of the present amendment, the status of the claims will be as follows:

1. (Currently amended) A method to determine gender of a canine subject, comprising contacting a nucleic acid sample from the canine subject with at least one ~~probe or~~ primer specific for a canine amelogenin gene, wherein one primer binds to a sequence of SEQ ID NO:22 and SEQ ID NO:23 and using the binding of the ~~at least one probe or~~ primers to detect a difference between the canine amelogenin gene on the Y chromosome and the canine amelogenin gene on the X chromosome, thereby determining gender of the canine subject.

2. (Canceled)

3. (Currently amended) The method of claim 1, wherein gender of the canine subject is determined by observing the presence of an amplification product as set forth in ~~contacting the nucleic acid sample with at least one probe or primer that specifically binds~~ SEQ ID NO:10 and/or SEQ ID NO:11.

4. (Currently amended) The method of claim 3, wherein gender of the canine subject is determined by contacting the nucleic acid sample with a primer pair, wherein a first primer of the primer pair ~~specifically~~ binds to SEQ ID NO:6 and/or SEQ ID NO:7 and a second primer of the primer pair ~~specifically~~ binds to SEQ ID NO:8 and/or SEQ ID NO:9.

5. (Original) The method of claim 4, wherein the first primer comprises at least 10 nucleotides of SEQ ID NO:3 and the second primer comprises at least 10 nucleotides of SEQ ID NO:5.

6. (Original) The method of claim 5, wherein the first primer is SEQ ID NO:3 and the second primer is SEQ ID NO:5.

7. (Original) The method of claim 5, wherein the first primer is SEQ ID NO:4 and the second primer is SEQ ID NO:5.

8. (Original) The method of claim 5, wherein the primer pair generates an amplification product that is a different length for the amelogenin gene on the X chromosome and the amelogenin gene on the Y chromosome.

9. (Currently amended) A method to determine gender of a canine subject, comprising contacting a nucleic acid sample from the canine subject with at least one probe or primer specific for canine amelogenin, wherein one primer binds to a sequence of SEQ ID NO:22 and SEQ ID NO:23 and detecting binding of the at least one probe or primer, thereby determining gender of the canine subject.

10. (Canceled)

11. (Currently amended) The method of claim 9, wherein gender of the canine subject is determined by contacting the nucleic acid sample with at least one ~~probe or primer pair~~ primer that ~~specifically binds SEQ ID NO:10 and/or SEQ ID NO:11.~~

12. (Currently amended) The method of claim 11, wherein gender of the canine subject is determined by contacting the nucleic acid sample with a primer pair, wherein a first primer of the primer pair ~~specifically~~ binds to SEQ ID NO:6 and/or SEQ ID NO:7 and a second primer of the primer pair ~~specifically~~ binds to SEQ ID NO:8 and/or SEQ ID NO:9.

13. (Original) The method of claim 9, wherein binding of the at least one probe or primer distinguishes the canine amelogenin gene on the X chromosome from the amelogenin gene on the Y chromosome.

Claims 14-22 (Cancelled)

23. (Currently amended) A method to detect binding of at least one primer ~~or probe~~ to a canine amelogenin gene, wherein one primer binds to a sequence of SEQ ID NO:22 and SEQ ID NO:23 comprising contacting a nucleic acid sample from a canine subject with at least one ~~probe or~~ primer specific for canine amelogenin.

24. (Canceled)

25. (Currently amended) The method of claim 23, wherein the nucleic acid sample is contacted with at least one ~~probe or primer pair~~ that ~~specifically binds~~ generates an amplification product as set forth in SEQ ID NO:10 ~~and/or~~ SEQ ID NO:11.

26. (Currently amended) The method of claim 25, wherein the nucleic acid sample is contacted with a primer pair, wherein a first primer of the primer pair ~~specifically~~ binds to SEQ ID NO:6 and/or SEQ ID NO:7 and a second primer of the primer pair ~~specifically~~ binds to SEQ ID NO:8 and/or SEQ ID NO:9.

Claims 27-35 (Cancelled)

36. (Currently amended) A method to genotype a canine subject, comprising contacting a nucleic acid sample from the canine subject with at least ~~one probe or~~ primer specific for canine amelogenin, wherein one primer binds to a sequence of SEQ ID NO:22 and SEQ ID NO:23 and detecting binding of the at least one probe or primer, thereby genotyping the canine subject.

37. (Canceled)

38. (Currently amended) The method of claim 36, wherein the nucleic acid sample is contacted with at least one ~~probe or~~ primer pair that specifically binds generates an amplification product as set forth in SEQ ID NO:10 and/or SEQ ID NO:11.

Claims 39-43 (Cancelled)

44. (Original) The method of claim 36, further comprising genotyping the canine subject at a microsatellite locus.

Claims 45-47 (Cancelled)

48. (Original) The method of claim 44, wherein the microsatellite locus is at least one of PEZ1/CATA1, PEZ3, PEZ5, PEZ6, PEZ8, PEZ10, PEZ11, PEZ12, PEZ13, PEZ15, PEZ16, PEZ17, PEZ20, PEZ21, FH2010, FH2054, and FH2079.

Claims 49-77 (Cancelled)

78. (New) The method of any of claims 1, 23 or 36, wherein the subject is canine familiaris.

79. (New) The method of any of claims 1, 23 or 36, wherein the subject is a domestic canine.

80. (New) The method of any of claims 11, 25, or 38, wherein the primer pair is SEQ ID NO:4 and SEQ ID NO:5.

81. (New) The method of any of claims 11, 25, or 38, wherein the primer pair is SEQ ID NO:3 and SEQ ID NO:5.